

2902076.3_Sequence Listing_ST25.txt
SEQUENCE LISTING

<110> Klinikum der Universitaet Muenchen
Strasburger, Christian J.

<120> Leptin Antagonist and Method for Quantitative Measurement of
Leptin

<130> 2902076.3

<140> US 10/579,203
<141> 2006-05-12

<150> PCT/EP2004/013043
<151> 2004-11-17

<150> Foreign National Application
<151> 2003-11-17

<160> 13

<170> PatentIn version 3.4

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Xaa His Asn Pro Ile Pro Met Pro Pro Ala Ala Ala Gly Leu Leu Leu
1 5 10 15

Leu Ala Ala Gln Pro Ala Met Ala Glu Leu Val Met Thr Gln Ser Pro
20 25 30

Lys Phe Met Ser Thr Ser Ile Gly Asp Arg Val Asn Ile Thr Cys Lys
35 40 45

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Ala Thr Gln Asn Val Arg Thr Ala Val Thr Trp Tyr Gln Gln Lys Pro
50 55 60

Gly Gln Ser Pro Gln Ala Leu Ile Phe Leu Ala Ser Asn Arg His Thr
65 70 75 80

Gly Val Pro Ala Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Thr Ile Asn Asn Val Lys Ser Glu Asp Leu Ala Asp Tyr Phe Cys
100 105 110

Leu Gln His Trp Asn Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu
115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
130 135 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
165 170 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
195 200 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
210 215 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys Xaa Xaa
225 230 235 240

Ser Arg Val Lys Arg Xaa Gln Ser Xaa Gly Gly Pro Gly Thr Pro Ile
245 250 255

Arg Pro Ile Gly Xaa Pro Tyr Tyr Asn Ser Leu Gly Gly Gly Phe Gln
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<210> 2
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Xaa	His	Asn	Pro	Ile	Pro	Met	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu		
1				5					10					15		

tta	ctc	gct	gcc	caa	cca	gcc	atg	gcc	gag	ctc	gtg	atg	acc	cag	tct	95
Leu	Leu	Ala	Ala	Gln	Pro	Ala	Met	Ala	Glu	Leu	Val	Met	Thr	Gln	Ser	
				20					25					30		

cca	aaa	ttc	atg	tcc	aca	tca	ata	gga	gac	agg	gtc	aat	atc	acc	tgc	143
Pro	Lys	Phe	Met	Ser	Thr	Ser	Ile	Gly	Asp	Arg	Val	Asn	Ile	Thr	Cys	
			35					40					45			

aag	gcc	act	cag	aat	gtt	cgt	act	gct	gtt	acc	tgg	tat	caa	cag	aaa	191
Lys	Ala	Thr	Gln	Asn	Val	Arg	Thr	Ala	Val	Thr	Trp	Tyr	Gln	Gln	Lys	
		50				55						60				

cca	ggg	cag	tct	cct	caa	gca	ctg	att	ttc	ttg	gca	tcc	aac	cgg	cac	239
Pro	Gly	Gln	Ser	Pro	Gln	Ala	Leu	Ile	Phe	Leu	Ala	Ser	Asn	Arg	His	
	65					70					75					

act	ggg	gtc	cct	gct	cga	ttc	aca	ggc	agt	gga	tct	ggg	aca	gat	ttc	287
Thr	Gly	Val	Pro	Ala	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
80					85				90					95		

act	ctc	acc	att	aac	aat	gtg	aaa	tct	gaa	gac	ctg	gca	gat	tat	ttc	335
Thr	Leu	Thr	Ile	Asn	Asn	Val	Lys	Ser	Glu	Asp	Leu	Ala	Asp	Tyr	Phe	
				100					105					110		

tgt	cta	caa	cat	tgg	aat	tat	cct	ctc	acg	ttc	ggc	tcg	ggg	aca	aag	383
Cys	Leu	Gln	His	Trp	Asn	Tyr	Pro	Leu	Thr	Phe	Gly	Ser	Gly	Thr	Lys	
			115					120					125			

ttg	gaa	ata	aaa	cgg	gct	gat	gct	gca	cca	act	gta	tcc	atc	ttc	cca	431
Leu	Glu	Ile	Lys	Arg	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	
		130					135					140				

cca	tcc	agt	gag	cag	tta	aca	tct	gga	ggg	gcc	tca	gtc	gtg	tgc	ttc	479
Pro	Ser	Ser	Glu	Gln	Leu	Thr	Ser	Gly	Gly	Ala	Ser	Val	Val	Cys	Phe	
	145					150					155					

ttg	aac	aac	ttc	tac	ccc	aaa	gac	atc	aat	gtc	aag	tgg	aag	att	gat	527
Leu	Asn	Asn	Phe	Tyr	Pro	Lys	Asp	Ile	Asn	Val	Lys	Trp	Lys	Ile	Asp	
160					165					170					175	

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ggc agt gaa cga caa aat ggc gtc ctg aac agt tgg act gat cag gac Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp 180 185 190	575
agc aaa gac agc acc tac agc atg agc agc acc ctc acg ttg acc aag Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys 195 200 205	623
gac gag tat gaa cga cat aac agc tat acc tgt gag gcc act cac aag Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys 210 215 220	671
aca tca act tca ccc att gtc aag agc ttc aac agg gga gag tgt tag Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys 225 230 235	719
taa tct aga gtt aag cgg ccg caa tcg agg ggg ggc ccg gta ccc caa Ser Arg Val Lys Arg Pro Gln Ser Arg Gly Gly Pro Val Pro Gln 240 245 250	767
ttc gcc cta tag ggg ngc cgt att aca att cac tgg gcg gcg gtt ttc Phe Ala Leu Gly Xaa Arg Ile Thr Ile His Trp Ala Ala Val Phe 255 260 265	815
aan Xaa	818

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Xaa His Asn Pro Ile Pro Met Pro Thr Ala Ala Ala Gly Leu Leu Leu 1 5 10 15
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Lys Phe Met Ser Thr Ser Ile Gly Asp Arg Val Asn Ile Thr Cys Lys 35 40 45
Ala Thr Gln Asn Val Arg Thr Ala Val Thr Trp Tyr Gln Gln Lys Pro 50 55 60
Gly Gln Ser Pro Gln Ala Leu Ile Phe Leu Ala Ser Asn Arg His Thr 65 70 75 80
Gly Val Pro Ala Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr 85 90 95

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Leu Thr Ile Asn Asn Val Lys Ser Glu Asp Leu Ala Asp Tyr Phe Cys
100 105 110

Leu Gln His Trp Asn Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu
115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
130 135 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
165 170 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
195 200 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
210 215 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

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Ser Arg Val Lys Arg Pro Gln Ser Arg Gly Gly Pro Val Pro Gln Phe
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Ala Leu

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<223> The 'Xaa' at location 13 stands for Lys, or Asn.

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Gly Xaa Arg Ile Thr Ile His Trp Ala Ala Val Phe Xaa
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<211> 292

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Val Ile Met Lys Tyr Leu Xaa Ala Tyr Gly Pro Ala Ala Gly Leu Leu
 20 25 30

Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Leu Glu Ser
 35 40 45

Gly Pro Gly Leu Val Ala Pro Ser Glu Ser Leu Ser Ile Thr Cys Thr
 50 55 60

Ile Ser Gly Phe Ser Leu Thr Asp Asp Gly Val Ser Trp Ile Arg Gln

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65          70          75          80
Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Gly Gly
      85          90          95
Ser Thr Tyr Phe Asn Ser Leu Phe Lys Ser Arg Leu Ser Ile Thr Arg
      100        105        110
Asp Asn Ser Lys Ser Gln Val Phe Leu Glu Met Asp Ser Leu Gln Thr
      115        120        125
Asp Asp Thr Ala Met Tyr Tyr Cys Ala Lys His Asp Gly His Glu Thr
      130        135        140
Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Lys
      145        150        155        160
Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln
      165        170        175
Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro
      180        185        190
Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val
      195        200        205
His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser
      210        215        220
Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys
      225        230        235        240
Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val
      245        250        255
Pro Arg Asp Cys Thr Ser His His His His His Xaa Ala Ser Leu
      260        265        270
Val Val Ala Val Ala Leu His Ser Phe Val Xaa Ile Lys Ala Asn Arg
      275        280        285
Arg Pro Ala Xaa
      290

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Leu Ala Xaa Arg Gly Gly Gly Arg Lys Ile Xaa Phe Xaa Arg Glu Thr	
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gtc ata atg aaa tac ctt ttn gcc tac ggg cca gcc gct gga ttg tta	96
Val Ile Met Lys Tyr Leu Xaa Ala Tyr Gly Pro Ala Ala Gly Leu Leu	
20 25 30	
tta ctc gct gcc caa cca gcc atg gcc cag gtg aaa ctg ctc gag tca	144
Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Leu Glu Ser	
35 40 45	
gga cct ggc ctg gtg gcg ccc tca gag agc ctg tcc atc aca tgc act	192
Gly Pro Gly Leu Val Ala Pro Ser Glu Ser Leu Ser Ile Thr Cys Thr	
50 55 60	
atc tca ggg ttc tca tta acc gac gat ggt gta agc tgg att cgg cag	240
Ile Ser Gly Phe Ser Leu Thr Asp Asp Gly Val Ser Trp Ile Arg Gln	
65 70 75 80	
cct cca gga aag ggt ctg gag tgg ctg gga gta ata tgg ggt ggt gga	288
Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Gly Gly	

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85

90

95

agc	aca	tac	ttt	aat	tca	ctt	ttc	aaa	tcc	aga	ctg	agc	atc	acc	agg	336
Ser	Thr	Tyr	Phe	Asn	Ser	Leu	Phe	Lys	Ser	Arg	Leu	Ser	Ile	Thr	Arg	
			100					105					110			
gac	aac	tct	aag	agc	caa	gtt	ttc	tta	gaa	atg	gac	agt	cta	caa	act	384
Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Leu	Glu	Met	Asp	Ser	Leu	Gln	Thr	
		115					120					125				
gat	gac	aca	gcc	atg	tac	tac	tgc	gcc	aaa	cat	gac	gga	cac	gag	act	432
Asp	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Ala	Lys	His	Asp	Gly	His	Glu	Thr	
		130				135					140					
atg	gac	tat	tgg	ggt	caa	gga	acc	tca	gtc	acc	gtc	tcc	tca	tcc	aaa	480
Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Ser	Lys	
145					150					155					160	
acg	aca	ccc	cca	tct	gtc	tat	cca	ctg	gcc	cct	gga	tct	gct	gcc	caa	528
Thr	Thr	Pro	Pro	Ser	Val	Tyr	Pro	Leu	Ala	Pro	Gly	Ser	Ala	Ala	Gln	
				165					170					175		
act	aac	tcc	atg	gtg	acc	ctg	gga	tgc	ctg	gtc	aag	ggc	tat	ttc	cct	576
Thr	Asn	Ser	Met	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	Pro	
			180					185					190			
gag	cca	gtg	aca	gtg	acc	tgg	aac	tct	gga	tcc	ctg	tcc	agc	ggt	gtg	624
Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Ser	Leu	Ser	Ser	Gly	Val	
		195					200					205				
cac	acc	ttc	cca	gct	gtc	ctg	cag	tct	gac	ctc	tac	act	ctg	agc	agc	672
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	
		210				215					220					
tca	gtg	act	gtc	ccc	tcc	agc	acc	tgg	ccc	agc	gag	acc	gtc	acc	tgc	720
Ser	Val	Thr	Val	Pro	Ser	Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	
225					230					235					240	
aac	gtt	gcc	cac	ccg	gcc	agc	agc	acc	aag	gtg	gac	aag	aaa	att	gtg	768
Asn	Val	Ala	His	Pro	Ala	Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Val	
				245					250					255		
ccc	agg	gat	tgt	act	agt	cat	cat	cat	cat	cat	cat	taa	gct	agc	cta	816
Pro	Arg	Asp	Cys	Thr	Ser	His	His	His	His	His	His		Ala	Ser	Leu	
			260					265						270		
gtg	gtg	gcg	gtg	gct	ctc	cat	tcg	ttt	gtg	ang	ata	aag	gcc	aat	cgn	864
Val	Val	Ala	Val	Ala	Leu	His	Ser	Phe	Val	Xaa	Ile	Lys	Ala	Asn	Arg	
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aga	cct	gcg	cna													876
Arg	Pro	Ala	Xaa													
			290													

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<223> The 'Xaa' at location 11 stands for Ile, Val, or Leu.

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<222> (13)..(13)

<223> The 'Xaa' at location 13 stands for Thr, Ala, Pro, or Ser.

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Val Ile Met Lys Tyr Leu Xaa Ala Tyr Gly Pro Ala Ala Gly Leu Leu
20 25 30

Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Leu Glu Ser
35 40 45

Gly Pro Gly Leu Val Ala Pro Ser Glu Ser Leu Ser Ile Thr Cys Thr
50 55 60

Ile Ser Gly Phe Ser Leu Thr Asp Asp Gly Val Ser Trp Ile Arg Gln
65 70 75 80

Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Gly Gly
85 90 95

Ser Thr Tyr Phe Asn Ser Leu Phe Lys Ser Arg Leu Ser Ile Thr Arg
100 105 110

Asp Asn Ser Lys Ser Gln Val Phe Leu Glu Met Asp Ser Leu Gln Thr
115 120 125

Asp Asp Thr Ala Met Tyr Tyr Cys Ala Lys His Asp Gly His Glu Thr
130 135 140

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Lys
145 150 155 160

Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln
165 170 175

Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro
180 185 190

Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val
195 200 205

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His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser
210 215 220

Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys
225 230 235 240

Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val
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Pro Arg Asp Cys Thr Ser His His His His His His
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Ala Asn Arg Arg Pro Ala Xaa
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Met Ala Gln Val Gln Leu
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1

5

cag	gag	tca	gga	act	gaa	gtg	gta	aag	cct	ggg	gct	tca	gtg	aag	ttg	103
Gln	Glu	Ser	Gly	Thr	Glu	Val	Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Leu	
			10					15					20			
tcc	tgc	aag	gct	tct	ggc	tac	atc	ttc	aca	agt	tat	gat	ata	gac	tgg	151
Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ile	Phe	Thr	Ser	Tyr	Asp	Ile	Asp	Trp	
		25					30					35				
gtg	agg	cag	acg	cct	gaa	cag	gga	ctt	gag	tgg	att	gga	tgg	att	ttt	199
Val	Arg	Gln	Thr	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Trp	Ile	Phe	
	40					45					50					
cct	gga	gag	ggg	agt	act	gaa	tac	aat	gag	aag	ttc	aag	ggc	agg	gcc	247
Pro	Gly	Glu	Gly	Ser	Thr	Glu	Tyr	Asn	Glu	Lys	Phe	Lys	Gly	Arg	Ala	
					60					65					70	
aca	ctg	agt	gta	gac	aag	tcc	tcc	agc	aca	gcc	tat	atg	gag	ctc	act	295
Thr	Leu	Ser	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Thr	
				75					80					85		
agg	ctg	aca	tct	gag	gac	tct	gct	gtc	tat	ttc	tgt	gct	aga	ggg	gac	343
Arg	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Gly	Asp	
			90					95					100			
tac	tat	agg	cgc	tac	ttt	gac	ttg	tgg	ggc	caa	ggg	acc	acg	gtc	acc	391
Tyr	Tyr	Arg	Arg	Tyr	Phe	Asp	Leu	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	
		105					110					115				
gtc	tcc	tca	tgt	gga	ggc	ggt	tca	ggc	gga	ggt	ggc	tct	ggc	ggt	ggc	439
Val	Ser	Ser	Cys	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
	120					125					130					
gga	tct	gac	att	gag	ctc	acc	cag	tct	cca	gca	atc	atg	tct	gca	tct	487
Gly	Ser	Asp	Ile	Glu	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala	Ser	
					140					145					150	
cca	ggg	gag	agg	gtc	acc	atg	acc	tgc	agt	gcc	agc	tca	agt	ata	cgt	535
Pro	Gly	Glu	Arg	Val	Thr	Met	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Ile	Arg	
				155				160						165		
tac	ata	tat	tgg	tac	caa	cag	aag	cct	gga	tcc	tcc	ccc	aga	ctc	ctg	583
Tyr	Ile	Tyr	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Arg	Leu	Leu	
			170					175					180			
att	tat	gac	aca	tcc	aac	gtg	gct	cct	gga	gtc	cct	ttt	cgc	ttc	agt	631
Ile	Tyr	Asp	Thr	Ser	Asn	Val	Ala	Pro	Gly	Val	Pro	Phe	Arg	Phe	Ser	
		185					190					195				
ggc	agt	ggg	tct	ggg	acc	tct	tat	tct	ctc	aca	atc	aac	cga	atg	gag	679
Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Asn	Arg	Met	Glu	
	200					205					210					
gct	gag	gat	gct	gcc	act	tat	tac	tgc	cag	gag	tgg	agt	ggt	tat	cct	727
Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Glu	Trp	Ser	Gly	Tyr	Pro	
					220					225					230	
ctc	acg	ttc	ggc	tcg	ggc	acc	aag	cgg	gaa	atc	aaa	cgg	gcg	gcc	gca	775
Leu	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Arg	Glu	Ile	Lys	Arg	Ala	Ala	Ala	
				235					240					245		
ggt	gcg	ccg	gtg	ccg	tat	ccg	gat	ccg	ctg	gaa	ccg	cgt	gccgcataga			824
Gly	Ala	Pro	Val	Pro	Tyr	Pro	Asp	Pro	Leu	Glu	Pro	Arg				
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<211> 259

<212> PRT

<213> Mus musculus

<400> 11

Met Ala Gln Val Gln Leu Gln Glu Ser Gly Thr Glu Val Val Lys Pro
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Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr
 20 25 30

Ser Tyr Asp Ile Asp Trp Val Arg Gln Thr Pro Glu Gln Gly Leu Glu
 35 40 45

Trp Ile Gly Trp Ile Phe Pro Gly Glu Gly Ser Thr Glu Tyr Asn Glu
 50 55 60

Lys Phe Lys Gly Arg Ala Thr Leu Ser Val Asp Lys Ser Ser Ser Thr
 65 70 75 80

Ala Tyr Met Glu Leu Thr Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr
 85 90 95

Phe Cys Ala Arg Gly Asp Tyr Tyr Arg Arg Tyr Phe Asp Leu Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Cys Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro
 130 135 140

Ala Ile Met Ser Ala Ser Pro Gly Glu Arg Val Thr Met Thr Cys Ser
 145 150 155 160

Ala Ser Ser Ser Ile Arg Tyr Ile Tyr Trp Tyr Gln Gln Lys Pro Gly
 165 170 175

Ser Ser Pro Arg Leu Leu Ile Tyr Asp Thr Ser Asn Val Ala Pro Gly
 180 185 190

Val Pro Phe Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
 195 200 205

Thr Ile Asn Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 210 215 220

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Glu Trp Ser Gly Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Arg Glu
225 230 235 240

Ile Lys Arg Ala Ala Ala Gly Ala Pro Val Pro Tyr Pro Asp Pro Leu
245 250 255

Glu Pro Arg

<210> 12
<211> 1252
<212> DNA
<213> Mus musculus

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gtgtaagctg gattcggcag cctccaggaa agggctctgga gtggctggga gtaatatggg 180
gtgggtggaag cacatacttt aattcacttt tcaaattccag actgagcatc accagggaca 240
actctaagag ccaagttttc ttagaaatgg acagtctaca aactgatgac acagccatgt 300
actactgcg caaacatgac ggacacgaga ctatggacta ttgggggtcaa ggaacctcag 360
tcaccgtctc ctcatccaaa acgacacccc catctgtcta tccactggcc cctggatctg 420
ctgccc aaac taactccatg gtgaccctgg gatgcctggg caagggctat ttccctgagc 480
cagtgcagat gacctggaac tctggatccc tgtccagcgg tgtgcacacc ttcccagctg 540
tcctgcagtc tgacctctac actctgagca gctcagtgac tgtcccctcc agcacctggc 600
ccagcgagac cgtcacctgc aacgttgccc acccggccag cagcaccaag gtggacaaga 660
aaattgtgcc cagggattgt actagtgggtg gcggaggtag tgggtggcga ggtagcgggtg 720
gcggagggtt tgggtggcga ggttccgaat tcctcgaggt gcccatccaa aaagtccaag 780
atgacaccaa aaccctcatc aagacaattg tcaccaggat caatgacatt tcacacacgc 840
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tcctgacctt atccaagatg gaccagacac tggcagtcta ccaacagatc ctccaccagta 960
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<210> 13
<211> 401
<212> PRT
<213> Mus musculus

<400> 13

Met Ala Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Ala Pro
 1 5 10 15

Ser Glu Ser Leu Ser Ile Thr Cys Thr Ile Ser Gly Phe Ser Leu Thr
 20 25 30

Asp Asp Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Leu Gly Val Ile Trp Gly Gly Gly Ser Thr Tyr Phe Asn Ser Leu
 50 55 60

Phe Lys Ser Arg Leu Ser Ile Thr Arg Asp Asn Ser Lys Ser Gln Val
 65 70 75 80

Phe Leu Glu Met Asp Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr
 85 90 95

Cys Ala Lys His Asp Gly His Glu Thr Met Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Ser Val Thr Val Ser Ser Ser Lys Thr Thr Pro Pro Ser Val Tyr
 115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
 130 135 140

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
 145 150 155 160

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
 180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
 195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Thr Ser Gly
 210 215 220

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 225 230 235 240

Gly Gly Ser Glu Phe Leu Glu Val Pro Ile Gln Lys Val Gln Asp Asp
 245 250 255

2902076.3_Sequence Listing_ST25.txt

Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser
260 265 270

His Thr Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe
275 280 285

Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr
290 295 300

Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val
305 310 315 320

Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val
325 330 335

Leu Ala Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu
340 345 350

Thr Leu Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr
355 360 365

Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu
370 375 380

Trp Gln Leu Asp Leu Ser Pro Gly Cys Thr Ser His His His His His
385 390 395 400

His